OIPE

#2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/964,666

DATE: 10/16/2001 TIME: 15:20:47

Input Set : A:\PTO.txt

Output Set: N:\CRF3\10162001\I964666.raw

```
SEQUENCE LISTING
```

```
(1) GENERAL INFORMATION:
             (i) APPLICANT: de la Monte, Suzanne
      6
      7
                            Wands, Jack R.
      9
            (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
     10
                                      Screening Drugs Effective for the Treatment or Prevention
                                      of Alzheimer's Disease
     11
     13
           (iii) NUMBER OF SEQUENCES: 14
            (iv) CORRESPONDENCE ADDRESS:
     15
     16
                  (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
     17
                  (B) STREET: 1100 New York Ave., Suite 600
     18
                  (C) CITY: Washington
     19
                  (D) STATE: DC
                                                                    ENTERED
     20
                  (E) COUNTRY: USA
     21
                  (F) ZIP: 20005-3934
     23
             (v) COMPUTER READABLE FORM:
     24
                  (A) MEDIUM TYPE: Floppy disk
     25
                  (B) COMPUTER: IBM PC compatible
     26
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     27
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     29
            (vi) CURRENT APPLICATION DATA:
                  (A) APPLICATION NUMBER: US/09/964,666
C--> 30
C--> 31
                  (B) FILING DATE: 28-Sep-2001
     32
                  (C) CLASSIFICATION:
     34
          (viii) ATTORNEY/AGENT INFORMATION:
     35
                  (A) NAME: Esmond, Robert W.
     36
                  (B) REGISTRATION NUMBER: 32,893
     37
                  (C) REFERENCE/DOCKET NUMBER: 0609.4370000
     39
            (ix) TELECOMMUNICATION INFORMATION:
                  (A) TELEPHONE: 202-371-2600
     40
                  (B) TELEFAX: 202-371-2540
        (2) INFORMATION FOR SEQ ID NO: 1:
     46
             (i) SEQUENCE CHARACTERISTICS:
     47
                  (A) LENGTH: 1442 base pairs
     48
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
     49
     50
                  (D) TOPOLOGY: both
     52
            (ii) MOLECULE TYPE: cDNA
            (ix) FEATURE:
     56
                  (A) NAME/KEY: CDS
     57
                  (B) LOCATION: 15..1:139
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     62 TTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC
                                                                                 50
     63
                        Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
     66 AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC
                                                                                 98
```

67 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/964,666

DATE: 10/16/2001 TIME: 15:20:47

Input Set : A:\PTO.txt

68 15			20		25				
70 GAT TCT CCT	GCC TCA	GCC TCC	CCA GTA	GCT GGG	ATT ACA	GGC	ATG '	TGC	146
71 Asp Ser Pro	Ala Ser	Ala Ser	Pro Val	Ala Gly	Ile Thr	Gly	Met	Cys	
72 30		35			40				
74 ACC CAC GCT									194
75 Thr His Ala	Arg Leu		Tyr Phe		Val Glu	Met	Glu		
76 45		50		55				60	0.4.0
78 CTC CAT GTT									242
79 Leu His Val 80	GIY GIN	Ala Giy	Leu Giu	70	Thr Ser	ASP	75	PIO	
82 TCC GTC TCG		САА АСТ	сст дсд		ልሮሞ ሮፎሮ	CAC		GCC	290
83 Ser Val Ser									250
84	80	· Der	85	111 1119	1111 017	90			
86 CGG CTC TGC		AAT TTT		AGA AAC	AGG GTT		CTG 2	ATG	338
87 Arg Leu Cys									
88 95			100	-	105				
90 TGC CCA AGC	TGG TCT	CCT GAG	CTC AAG	CAG TCC	ACC TGC	CTC	AGC	CTC	386
91 Cys Pro Ser	Trp Ser	Pro Glu	Leu Lys	Gln Ser	Thr Cys	Leu	Ser :	Leu	
92 110		115			120				
94 CCA AAG TGC	TGG GAT	TAC AGG	CGT GCA	GCC GTG	CCT GGC	CTT	TTT	ATT	434
95 Pro Lys Cys	Trp Asp	Tyr Arg	Arg Ala	Ala Val	Pro Gly	Leu	Phe	Ile	
96 125		130		135				140	
98 TTA TTT TTT									482
99 Leu Phe Phe			Cys Pro		Thr Gln	Asp		Val	
100	145			150			155		
ווויס כאב ייובב ייובי									
					ACT CCT				530
103 Gln Trp Cy	s Asp His		Leu Glr	n Pro Ser		o Glu	Ile		530
103 Gln Trp Cy 104	s Asp His 160	s Ser Ser	Leu Glr 165	n Pro Ser 5	Thr Pro	Glu 170	Ile	Lys	
103 Gln Trp Cy 104 106 CAT CCT CC	S Asp His 160 I GCC TC	Ser Ser	Leu Glr 169 CAA GTA	n Pro Ser 5 A GCT GGG	Thr Pro	Glu 170 A GAC	Ile ATG	Lys CAC	530 578
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr	s Asp His 160 T GCC TCA o Ala Ser	Ser Ser	Leu Glr 165 CAA GTA Gln Val	n Pro Ser 5 A GCT GGG	Thr Pro ACC AAI Thr Lys	Glu 170 A GAC S Asp	Ile ATG	Lys CAC	
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108	s Asp His 160 I GCC TCA D Ala Ser 5	S Ser Ser A GCC TCC T Ala Ser	Leu Glr 165 CCAA GTA Gln Val	n Pro Ser 5 A GCT GGG L Ala Gly	Thr Pro G ACC AAA Thr Lys 185	Glu 170 A GAC S Asp	Ile ATG Met	Lys CAC His	578
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108 17 110 CAC TAC AC	S Asp His 160 T GCC TCA D Ala Ser 5 C TGG CTA	S Ser Ser GCC TCC Ala Ser ATT TTT	Leu Glr 165 CAA GTA Gln Val 180	n Pro Ser 5 A GCT GGG L Ala Gly	Thr Pro ACC AAA Thr Lys 185	Glu 170 A GAC B Asp T TTG	Ile ATG Met	Lys CAC His CAG	
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108	S Asp His 160 T GCC TCA D Ala Ser 5 C TGG CTA	S Ser Ser GCC TCC Ala Ser ATT TTT	Leu Glr 169 C CAA GTA Gln Val 180 C ATT TT E Ile Phe	n Pro Ser 5 A GCT GGG L Ala Gly	Thr Pro ACC AAA Thr Lys 185	Glu 170 A GAC B Asp T TTG	Ile ATG Met	Lys CAC His CAG	578
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108 17 110 CAC TAC AC 111 His Tyr Th	S Asp His 160 I GCC TCF O Ala Ser C TGG CTF r Trp Let	S Ser Ser A GCC TCC A ALA Ser A ATT TTT I Ile Phe 195	C CAA GTA C Gln Val 180 C ATT TT	n Pro Ser 5 A GCT GGG L Ala Gly T ATT TTT e Ile Phe	G ACC AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Glu 170 A GAC B Asp T TTG E Leu	Ile ATG Met AGA Arg	Lys CAC His CAG Gln	578
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108 17 110 CAC TAC AC 111 His Tyr Th 112 190	S Asp His 160 I GCC TCF O Ala Ser C TGG CTF T Trp Leu C TCT GTC	S Ser Ser A GCC TCC A ATT TTT A Ile Phe 195 C ACC CACC	C CAA GTA C GIn Val 180 C ATT TTT C Ile Phe	A GCT GGG A GCT GGG A ATT TTT E ILE Phe	Thr Pro ACC AAA Thr Lys 185 AAT TTT AAN Phe 200 TGG CGG	O Glu 170 A GAC S Asp T TTG E Leu	ATG Met AGA Arg	CAC His CAG Gln	578 626
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108 17 110 CAC TAC AC 111 His Tyr Th 112 190 114 AGT CTC AA	S Asp His 160 I GCC TCF O Ala Ser C TGG CTF T Trp Leu C TCT GTC	S Ser Ser A GCC TCC A ATT TTT A Ile Phe 195 C ACC CACC	C CAA GTA C GIn Val 180 C ATT TTT C Ile Phe	A GCT GGG A GCT GGG A ATT TTT E ILE Phe	Thr Pro ACC AAA Thr Lys 185 AAT TTT ASn Phe 200 TGG CGG	O Glu 170 A GAC S Asp T TTG E Leu	ATG Met AGA Arg	CAC His CAG Gln	578 626
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108 17 110 CAC TAC AC 111 His Tyr Th 112 190 114 AGT CTC AA 115 Ser Leu As	S Asp His 160 I GCC TCA D Ala Ser TTG CTA TTP Let C TCT GTC A Ser Val	GCC TCC A GCC TCC A ATT TTT A Ile Phe 195 C ACC CAC Thr Glr 210	C CAA GTA C CAA GTA C Gln Val 180 C ATT TTT C Ile Phe	n Pro Ser G GCT GGG L Ala Gly T ATT TTT E Ile Phe A GTG CAG 7 Val Glr 215	Thr Pro ACC AAA Thr Lys 185 AAT TTT ASn Phe 200 TGG CGG TTP Arg	Glu 170 A GAC S Asp T TTG E Leu C AAT J Asn	ATG Met AGA Arg CTT Leu	Lys CAC His CAG Gln GGC Gly 220	578 626
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108	S Asp His 160 F GCC TCA O Ala Ser TTG CTA TTP Let C TCT GTC A SCT Val	G Ser Ser A GCC TCC A ATT TTT A Ile Phe 195 C ACC CAC Thr Glr 210 G CCT CCC	C CAA GTA C CAA GTA C GIN Val 180 C ATT TTT C Ile Phe G GCT GGA Ala Gly	A GTG CAG Val GAG TAG AGTG CAG AGT AGTG CAG AGT AGT AGT AGT AGT AGT AGT AGT AGT A	Thr Pro ACC AAA Thr Lys 185 AAT TTT ASn Phe 200 TGG CGG TTP Arg	Glu 170 A GAC S Asp T TTG E Leu C AAT Asn	ATG Met AGA Arg CTT Leu CCC	Lys CAC His CAG Gln GGC Gly 220 AGC	578 626 674
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108	S Asp His 160 F GCC TCA O Ala Ser TTG CTA TTP Leu C TCT GTC A SCT Val	G Ser Ser A GCC TCC A ATT TTT A Ile Phe 195 C ACC CAC Thr Glr 210 G CCT CCC	C CAA GTA C CAA GTA C GIN Val 180 C ATT TTT C Ile Phe G GCT GGA Ala Gly	A GTG CAG Val GAG TAG AGTG CAG AGT AGTG CAG AGT AGT AGT AGT AGT AGT AGT AGT AGT A	Thr Pro ACC AAA Thr Lys 185 AAT TTT ASn Phe 200 TGG CGG TTP Arg	Glu 170 A GAC S Asp T TTG E Leu C AAT Asn	ATG Met AGA Arg CTT Leu	Lys CAC His CAG Gln GGC Gly 220 AGC	578 626 674
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108	S ASP His 160 I GCC TCF O Ala Ser TTP Let C TCT GTC O Ser Val A CCT CTC O Pro Let 225 I AGC TGC	G Ser Ser A GCC TCC A ATT TTT I Ile Phe 195 C ACC CAC Thr Glr 210 G CCT CCC I Pro Pro G GAC TAC	Leu Glr 169 C CAA GTA 180 T ATT TTT L Ile Phe G GCT GGA Ala Gly C GGG TTC C GJy Phe C AGG CGC	A GTG CAG Val Glr AAG TTA C AAG TTA C AAG TTA C AAG CAG C AAG CAG C CCA CCA	Thr Pro ACC AAA Thr Lys 185 AAT TTT ASn Phe 200 TGG CGG Trp Arg TTC TCG Phe Sei	Glu 170 A GAC A SP TTTG Leu C AAT A Sn C TGC C Cys	ATG Met AGA Arg CTT Leu CCC Pro 235 AAT	Lys CAC His CAG Gln GGC Gly 220 AGC Ser	578 626 674
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108	S ASP His 160 I GCC TCF Ala Ser TTP Let TTP Let A CCT CTC A Pro Let 225 I AGC TGG T Ser Trp	G Ser Ser A GCC TCC A ATT TTT I Ile Phe 195 C ACC CAC Thr Glr 210 G CCT CCC I Pro Pro G GAC TAC	Leu Glr 169 C CAA GTA Gln Val 180 T ATT TTT E Ile Phe G GCT GGA Ala Gly C GGG TTC C GGG TTC C GAG CGC C Arg Arg	A GCT GGG A TTTTT E ILE Phe A GTG CAG Y Val Glr 215 C AAG TTA E Lys Leu 230 C CCA CCA	Thr Pro ACC AAA Thr Lys 185 AAT TTT ASn Phe 200 TGG CGG Trp Arg TTC TCG Phe Sei	Glu 170 A GAC A SP TTTG E Leu C AAT G Asn C TGC C Cys A GCT	ATG Met AGA Arg CTT Leu CCC Pro 235 AAT Asn	Lys CAC His CAG Gln GGC Gly 220 AGC Ser	578 626 674 722
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108	S ASP His 160 I GCC TCF O Ala Ser C TGG CTF T Trp Let C TCT GTC A CCT CTC A CCT CTC A CCT CTC A CCT CTC T AGC TGG T Ser Trp 240	GCC TCC ALA SET ATT TTT I I LE Phe 195 CACC CAC Thr Glr 210 GCCT CCC FPO Pro GGAC TAC OASP TYT	Leu Glr 169 C CAA GTA Gln Val 180 T ATT TTT E Ile Phe G GCT GGA Ala Gly C GGG TTC C GGG TTC C AGG CGC ATG ATG 249	A GCT GGG A TTTTT E ILE Phe A GTG CAG Y Val Glr 215 C AAG TTA E Lys Leu 230 C CCA CCA	Thr Pro ACC AAA Thr Lys 185 AAT TTT AAA Phe 200 TGG CGG TTP Arg TTC TCG A TTC TCG	Glu 170 A GAC A SP TTTG E Leu C AAT J Asn C TGC C Cys A GCT 1 Ala 250	ATG Met AGA Arg CTT Leu CCC Pro 235 AAT Asn	Lys CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe	578 626 674 722 770
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108	S ASP His 160 I GCC TCF Ala Ser TTP Let TTP Let A CCT CTC PTO Let A CCT CTC A PTO Let C PTO Let C PTO Let C TGC TGC A CT TTC A CT	GCC TCC ATT TTT I I Phe 195 ACC CAC Thr Glr 210 GCCT CCC Pro Pro GGAC TAC ASp Tyr	Leu Glr 169 C CAA GTA Gln Val 180 C ATT TTT C Ile Phe G GCT GGA Ala Gly C GGG TTC C GGG TTC C AGG CGC C Arg Arg 249 G GGG TTC	A GCT GGG A GTT TTT E Ile Phe A GTG CAG Y Val Glr 215 C AAG TTA E Lys Leu 230 C CCA CCA G Pro Pro C ACC ATG	Thr Pro ACC AAA Thr Lys 185 AAT TTT AAA TTC TCC TTC TCC A TTC TCC	Glu 170 A GAC A SP TTTG Leu C AAT J Asn C TGC C Cys A GCT A Ala 250 C AGG	ATG Met AGA Arg CTT Leu CCC Pro 235 AAT Asn	Lys CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe	578 626 674 722
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108	S ASP His 160 I GCC TCF Ala Ser TTP Let TTP Let C TCT GTC A SCT Val A CCT CTC A Pro Let 225 I AGC TGC TTP 240 I TTA GTF E Let Val	GCC TCC ATT TTT I I Phe 195 ACC CAC Thr Glr 210 GCCT CCC Pro Pro GGAC TAC ASp Tyr	Leu Glr 169 C CAA GTA Gln Val 180 C ATT TTT C Ile Phe G GCT GGA Ala Gly C GGG TTC C GGG TTC C AGG CGC C GGG TTC	A GCT GGG A GTT TTT E Ile Phe A GTG CAG Y Val Glr 215 C AAG TTA E Lys Leu 230 C CCA CCA G Pro Pro C ACC ATG	Thr Pro ACC AAA Thr Lys 185 AAT TTT AAAN Phe 200 GTGG CGG Trp Arg A TTC TCC	Glu 170 A GAC A ASP TTTG E Leu C AAT J ASN C TGC C Cys A GCT A Ala 250 C AGG A Arg	ATG Met AGA Arg CTT Leu CCC Pro 235 AAT Asn	Lys CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe	578 626 674 722 770
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108 17 110 CAC TAC AC 111 His Tyr Th 112 190 114 AGT CTC AA 115 Ser Leu As 117 205 119 TCA CTG CA 120 Ser Leu Gl 121 123 CTC CTG AG 124 Leu Leu Se 125 127 TTT GTA TT 128 Phe Val Ph 129	S ASP His 160 I GCC TCF Ala Ser TTP Leu C TCT GTC A Ser Val A CCT CTC A Pro Leu 225 I AGC TGC TGC TGC TTR 240 I TTA GTF E Leu Val 5	GCC TCC ATT TTT I I Phe 195 ACC CAC Thr Glr 210 GCT CCC Pro Pro GGAC TAC ASp Tyr A GAG ATC	Leu Glr 169 C CAA GTA Gln Val 180 C ATT TTT C Ile Phe G GCT GGA Ala Gly C AGG CGC Arg Arg Arg G GGG TTC C GGY Phe C AGG CGC C	A GCT GGG A ATT TTT E ILE Phe A GTG CAG Val Glr 215 C AAG TTA E Lys Leu 230 C CCA CCA G Pro Pro C ACC ATG	Thr Pro ACC AAA ATTT AAAT TTT AAAT TTT ACC ATTC TCC ATTC	Glu 170 A GAC A ASP TTG Leu C AAT J ASN C TGC C Cys A GCT A Ala 250 A Arg A Arg	ATG Met AGA Arg CTT Leu CCC Pro 235 AAT Asn TTG Leu	CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe ATC Ile	578 626 674 722 770 818
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108 17 110 CAC TAC AC 111 His Tyr Th 112 190 114 AGT CTC AA 115 Ser Leu As 117 205 119 TCA CTG CA 120 Ser Leu Gl 121 123 CTC CTG AG 124 Leu Leu Se 125 127 TTT GTA TT 128 Phe Val Ph 129 25 131 TTG ATC TC	S ASP His 160 I GCC TCF C Ala Ser C TGG CTF T Trp Leu C TCT GTC A CCT CTC A CTC CTC A CCT CTC A CTC CTC A CCT CTC A	GCC TCC ATT TTT I I Phe 195 ACC CAC Thr Glr 210 GCT CCC ASP Tyr A GAG ATC	Leu Glr 169 C CAA GTA Gln Val 180 C ATT TTT C Ile Phe G GCT GGA Ala Gly C AGG CGC Arg Arg Arg C GGG TTC C Gly Phe C GGY Phe C GGG TTC C GIY CCT	A GCT GGG A GTG CAG Val Glr A GTG CAG Val Glr 215 C AAG TTA E Lys Leu 230 C CCA CCA C CAC	Thr Pro ACC AAA ATTT ASS AAT TTT ASS ATTC TCC AT	Glu 170 A GAC A ASP TTG Leu C AAT A SA C TGC C CYS A GCT A Ala 250 C AGG A Arg C CAA	Ile ATG Met AGA Arg CTT Leu CCC Pro 235 AAT Asn TTG Leu AGT	CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe ATC Ile GCT	578 626 674 722 770
103 Gln Trp Cy 104 106 CAT CCT CC 107 His Pro Pr 108 17 110 CAC TAC AC 111 His Tyr Th 112 190 114 AGT CTC AA 115 Ser Leu As 117 205 119 TCA CTG CA 120 Ser Leu Gl 121 123 CTC CTG AG 124 Leu Leu Se 125 127 TTT GTA TT 128 Phe Val Ph 129	S ASP His 160 I GCC TCF C Ala Ser C TGG CTF T Trp Leu C TCT GTC A CCT CTC A CTC CTC A CCT CTC A CTC CTC A CCT CTC A	GCC TCC ATT TTT I I Phe 195 ACC CAC Thr Glr 210 GCT CCC ASP Tyr A GAG ATC	Leu Glr 169 C CAA GTA Gln Val 180 C ATT TTT C Ile Pho G GCT GGA Ala Gly C AGG CGC C AGG TTC C Gly Pho C CTG CCT C CTG CCT C CTG CCT C Leu Pro	A GCT GGG A GTG CAG Val Glr A GTG CAG Val Glr 215 C AAG TTA E Lys Leu 230 C CCA CCA C CAC	Thr Pro ACC AAA ATTT ASS AAT TTT ASS ATTC TCC AT	Glu 170 A GAC A ASP TTG Leu C AAT A SA C TGC C CYS A GCT A Ala 250 C AGG A Arg C CAA	Ile ATG Met AGA Arg CTT Leu CCC Pro 235 AAT Asn TTG Leu AGT	CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe ATC Ile GCT	578 626 674 722 770 818

RAW SEQUENCE LISTING DATE: 10/16/2001 PATENT APPLICATION: US/09/964,666 TIME: 15:20:47

Input Set : A:\PTO.txt

135																	
	GGG	ATT	ACA	GGC	GTG	AGC	CAC	CAC	GCC	CGG	CTT	ATT	TTT	AAT	TTT	TGT	914
136	Gly	Ile	Thr	Gly	Val	Ser	His	His	Ala	Arg	Leu	Ile	Phe	Asn	Phe	Cys	
	285					290					295					300	
															CAA		962
140	Leu	Phe	Glu	Met		Ser	His	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	
141					305					310					315		ı
															CGA		1010
	Pro	Asn	Leu	_	Ser	Leu	Gln	Pro		Pro	Pro	Gly	Leu	_	Arg	Phe	
145	maa			320					325	~~ =			~~ ~	330	~~~	~~~	1050
																CCA	1058
	ser	Cys	335	ser	ьeu	PIO	ser		тгр	Asp	туг	GIA	345	Leu	Pro	Pro	
149	CAC	CCC		אאת	ատա	መረመ	አ ጠጠ	340	y mm	7 C 7	CCC	ccc		መሮአ	CCA		1106
															Pro		1100
153	1115	350	ALG	VOII	FILE	СуБ	355	FIIC	116	AIG	Gry	360	Val	361	110	TYL	
	ጥጥር		GGC	TGG	ጥርጥ	CAA		ССТ	GAC	СТС	AGG		יררם (יריי מ	3.C.C.T.C	CAGCCT	1159
								Pro				10110	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	,,,,		2110001	1100
	365		1			370					375						
		AAAG!	rgc :	rggg <i>i</i>	ATTA		CGT	GAGC	CAC	CTCA		GCC	GCT	AAT :	TTAG!	AAAAT	1219
																IGGCTT	1279
163	CATO	GCAA!	rcc :	TTCC	AAAT	GA GO	CAC	AACA	CC	AGCC	AGTC	ACA'	TTT:	TA A	AACAG	STTACA	1339
165	TCT	TTAT:	TTT A	AGTA:	ract <i>i</i>	AG A	AAGT	AATAC	C AA	raaa(CATG	TCA	ACC!	rgc A	AAAT	CAGTA	1399
167	GTA	ACAG	AGT :	rctt:	TAT	AA C	CTTT	AAAC	AA A	GCTT:	ľAGA	GCA					1442
170	(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	NO: 2	2:								
172		(i) SE	QUENC	CE CE	HARAC	CTER:	ISTIC	cs:								
173			•	•				nino		ds							
175			(I	3) T	YPE:	amir	no ac	cid		ds							
175 176			(I (I) T (C) (C	PE:	amir DGY:	no ac line	cid ear		ds							
175 176 178		-	I) I) IOM (B) TY D) TO LECUI	PE: OPOLO LE T	amir DGY: YPE:	no ad line prot	cid ear tein	acio								
175 176 178 180		(xi	(I (I) MOI) SE(B) TY D) TO LECUI QUENO	PE: OPOLO LE TI CE DI	amir DGY: YPE: ESCRI	no ad line prot IPTIC	cid ear tein ON: S	acio	ID N O			•		21-	7 1.	
175 176 178 180 182	Met	(xi	(I (I) MOI) SE(B) TY D) TO LECUI QUENO	PE: POLO LE TY CE DI Leu	amir DGY: YPE: ESCRI	no ad line prot IPTIC	cid ear tein ON: S	acio	ID NO Leu			Asn	Gly	Ala	Ile	
175 176 178 180 182 183	Met 1	(xi Glu	(I (I) MOI) SE(Phe	3) TY D) TO LECUI QUENO Ser	PE: DPOLO LE TY CE DI Leu 5	amir DGY: YPE: ESCRI Leu	line prot PTIC Leu	cid ear tein DN: S Pro	acio SEQ :	ID NO Leu 10	Glu	Cys		_	15		
175 176 178 180 182 183 185	Met 1	(xi Glu	(I (I) MOI) SE(Phe	3) TY D) TO LECUI QUENC Ser Arg	PE: DPOLO LE TY CE DI Leu 5	amir DGY: YPE: ESCRI Leu	line prot PTIC Leu	cid ear tein DN: S Pro	SEQ :	ID NO Leu 10	Glu	Cys		Ser			
175 176 178 180 182 183 185	Met 1 Ser	(xi Glu Ala	(I (I) MOI) SE(Phe His	B) TY D) TO LECUI QUENO Ser Arg 20	PE: POLO LE TY CE DI Leu 5 Asn	amir DGY: YPE: ESCRI Leu Leu	no ac line prot IPTIC Leu Arg	cid ear tein ON: S Pro Leu	SEQ : Arg Pro 25	ID NO Leu 10 Gly	Glu Ser	Cys Ser	Asp	Ser 30	15 Pro	Ala	
175 176 178 180 182 183 185 186	Met 1 Ser	(xi Glu Ala	(I (I) MOI) SEC Phe His Ser	B) TY D) TO LECUI QUENO Ser Arg 20	PE: POLO LE TY CE DI Leu 5 Asn	amir DGY: YPE: ESCRI Leu Leu	no ac line prot IPTIC Leu Arg	cid ear tein DN: S Pro Leu	SEQ : Arg Pro 25	ID NO Leu 10 Gly	Glu Ser	Cys Ser	Asp Thr	Ser 30	15	Ala	
175 176 178 180 182 183 185 186 188	Met 1 Ser	(xi Glu Ala Ala	(I (I) MOI) SEC Phe His Ser 35	B) TY D) TO LECUI QUENC Ser Arg 20 Pro	YPE: DPOLO LE TY CE DI Leu 5 Asn	amir DGY: YPE: ESCRI Leu Leu	no ac line prod IPTIC Leu Arg	cid ear tein ON: S Pro Leu Ile 40	SEQ : Arg Pro 25 Thr	ID NO Leu 10 Gly Gly	Glu Ser Met	Cys Ser Cys	Asp Thr 45	Ser 30 His	15 Pro Ala	Ala Arg	
175 176 178 180 182 183 185 186 188	Met 1 Ser	(xi Glu Ala Ala	(I (I) MOI) SEC Phe His Ser 35	B) TY D) TO LECUI QUENC Ser Arg 20 Pro	YPE: DPOLO LE TY CE DI Leu 5 Asn	amir DGY: YPE: ESCRI Leu Leu	no ac line prod IPTIC Leu Arg	cid ear tein ON: S Pro Leu Ile 40	SEQ : Arg Pro 25 Thr	ID NO Leu 10 Gly Gly	Glu Ser Met	Cys Ser Cys	Asp Thr 45	Ser 30 His	15 Pro	Ala Arg	
175 176 178 180 182 183 185 186 188 189 191	Met 1 Ser Ser	(xi Glu Ala Ala Ile 50	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (Arg Pro	YPE: OPOLO LE TY CE DI Leu 5 Asn Val	amir DGY: YPE: ESCRI Leu Leu Ala	line prot IPTIC Leu Arg Gly Leu 55	cid ear tein DN: S Pro Leu Ile 40 Val	SEQ : Arg Pro 25 Thr	ID NO Leu 10 Gly Gly Met	Glu Ser Met Glu	Cys Ser Cys Phe 60	Asp Thr 45 Leu	Ser 30 His	15 Pro Ala Val	Ala Arg Gly	
175 176 178 180 182 183 185 186 188 189 191 192	Met 1 Ser Ser	(xi Glu Ala Ala Ile 50	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (Arg Pro	YPE: OPOLO LE TY CE DI Leu 5 Asn Val	amir DGY: YPE: ESCRI Leu Leu Ala	line prot IPTIC Leu Arg Gly Leu 55	cid ear tein DN: S Pro Leu Ile 40 Val	SEQ : Arg Pro 25 Thr	ID NO Leu 10 Gly Gly Met	Glu Ser Met Glu	Cys Ser Cys Phe 60	Asp Thr 45 Leu	Ser 30 His	15 Pro Ala	Ala Arg Gly	
175 176 178 180 182 183 185 186 189 191 192 194 195	Met 1 Ser Ser Leu Gln 65	(xi Glu Ala Ala Ile 50 Ala	(I (I) MOI) SEC Phe His Ser 35 Leu Gly	Arg Pro Tyr Leu	PPE: DPOLC DPOLC LE TY LE DI Leu 5 Asn Val Phe Glu	amir DGY: YPE: ESCRI Leu Leu Ala Phe Leu 70	line protection Leu Arg Gly Leu 55 Pro	cid ear tein DN: S Pro Leu Ile 40 Val	Acid Arg Pro 25 Thr Glu Ser	ID NO Leu 10 Gly Gly Met	Glu Ser Met Glu Asp 75	Cys Ser Cys Phe 60 Pro	Asp Thr 45 Leu Ser	Ser 30 His Wal	15 Pro Ala Val Ser	Ala Arg Gly Ala 80	
175 176 178 180 182 183 185 186 189 191 192 194 195	Met 1 Ser Ser Leu Gln 65	(xi Glu Ala Ala Ile 50 Ala	(I (I) MOI) SEC Phe His Ser 35 Leu Gly	Arg Pro Tyr Leu	PPE: DPOLC DPOLC LE TY LE DI Leu 5 Asn Val Phe Glu	amir DGY: YPE: ESCRI Leu Leu Ala Phe Leu 70	line protection Leu Arg Gly Leu 55 Pro	cid ear tein DN: S Pro Leu Ile 40 Val	Acid Arg Pro 25 Thr Glu Ser	ID NO Leu 10 Gly Gly Met	Glu Ser Met Glu Asp 75	Cys Ser Cys Phe 60 Pro	Asp Thr 45 Leu Ser	Ser 30 His Wal	15 Pro Ala Val	Ala Arg Gly Ala 80	
175 176 178 180 182 183 185 186 188 191 192 194 195 197	Met 1 Ser Ser Leu Gln 65 Ser	(xi Glu Ala Ala Ile 50 Ala Gln	(I (I) MOI) SEC Phe His Ser 35 Leu Gly Ser	Arg Pro Tyr Leu Ala	PPE: DPOLC DPOLC LE TY LE DI Leu 5 Asn Val Phe Glu Arg 85	amir DGY: YPE: ESCRI Leu Leu Ala Phe Leu 70	line protection and protection arg Gly Leu 55 Pro	cid ear tein DN: S Pro Leu Ile 40 Val Thr	SEQ : Arg Pro 25 Thr Glu Ser	ID No Leu 10 Gly Gly Met Asp His 90	Glu Ser Met Glu Asp 75	Cys Ser Cys Phe 60 Pro	Asp Thr 45 Leu Ser	Ser 30 His Wal	15 Pro Ala Val Ser Cys	Ala Arg Gly Ala 80 Leu	
175 176 178 180 182 183 185 186 188 191 192 194 195 197 198 200 201	Met 1 Ser Ser Leu Gln 65 Ser	(xi Glu Ala Ala Ile 50 Ala Gln Asn	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (Arg 20 Pro Tyr Leu Ala Cys 100	PPE: DPOLCE DPOLCE TY CE DF Leu 5 Asn Val Phe Glu Arg 85 Gly	amir DGY: YPE: ESCRI Leu Leu Ala Phe Leu 70 Tyr Arg	line protection and protection arg Gly Leu 55 Pro Arg	cid ear tein ON: S Pro Leu Ile 40 Val Thr Thr	Pro 25 Thr Glu Ser Gly Val 105	ID NO Leu 10 Gly Gly Met Asp His 90 Ser	Glu Ser Met Glu Asp 75 His Leu	Cys Ser Cys Phe 60 Pro Ala Met	Asp Thr 45 Leu Ser Arg Cys	Ser 30 His Wal Leu Pro 110	15 Pro Ala Val Ser Cys 95 Ser	Ala Arg Gly Ala 80 Leu Trp	
175 176 178 180 182 183 185 186 188 189 191 192 194 195 197 198 200 201 203	Met 1 Ser Ser Leu Gln 65 Ser	(xi Glu Ala Ala Ile 50 Ala Gln Asn	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (Arg 20 Pro Tyr Leu Ala Cys 100	PPE: DPOLCE DPOLCE TY CE DF Leu 5 Asn Val Phe Glu Arg 85 Gly	amir DGY: YPE: ESCRI Leu Leu Ala Phe Leu 70 Tyr Arg	line protection and protection arg Gly Leu 55 Pro Arg	cid ear tein ON: S Pro Leu Ile 40 Val Thr Thr Arg	Pro 25 Thr Glu Ser Gly Val 105	ID NO Leu 10 Gly Gly Met Asp His 90 Ser	Glu Ser Met Glu Asp 75 His Leu	Cys Ser Cys Phe 60 Pro Ala Met	Asp Thr 45 Leu Ser Arg Cys	Ser 30 His Wal Leu Pro 110	15 Pro Ala Val Ser Cys 95	Ala Arg Gly Ala 80 Leu Trp	
175 176 178 180 182 183 185 186 188 191 192 194 195 197 198 200 201 203 204	Met 1 Ser Ser Leu Gln 65 Ser Ala	(xi Glu Ala Ala Ile 50 Ala Gln Asn	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (Arg 20 Pro Tyr Leu Ala Cys 100 Leu	PE: PPOLO POLO LE TY LE DI Leu 5 Asn Val Phe Glu Arg 85 Gly Lys	amir DGY: YPE: ESCRI Leu Leu Ala Phe Leu 70 Tyr Arg Gln	line protection and protection arg Gly Leu 55 Pro Arg Asn Ser	cid ear tein ON: S Pro Leu Ile 40 Val Thr Thr Arg	Pro 25 Thr Glu Ser Gly Val 105 Cys	ID NO Leu 10 Gly Gly Met Asp His 90 Ser Leu	Glu Ser Met Glu Asp 75 His Leu Ser	Cys Ser Cys Phe 60 Pro Ala Met Leu	Asp Thr 45 Leu Ser Arg Cys Pro 125	Ser 30 His Val Leu Pro 110 Lys	15 Pro Ala Val Ser Cys 95 Ser Cys	Ala Arg Gly Ala 80 Leu Trp	
175 176 178 180 182 183 185 186 188 189 191 192 194 195 197 198 200 201 203 204 206	Met 1 Ser Ser Leu Gln 65 Ser Ala	(xi Glu Ala Ala Ile 50 Ala Gln Asn Pro	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (Arg 20 Pro Tyr Leu Ala Cys 100 Leu	PE: PPOLO POLO LE TY LE DI Leu 5 Asn Val Phe Glu Arg 85 Gly Lys	amir DGY: YPE: ESCRI Leu Leu Ala Phe Leu 70 Tyr Arg Gln	lo ad line protection and protection arg Gly Leu 55 Pro Arg Asn Ser Val	cid ear tein ON: S Pro Leu Ile 40 Val Thr Thr Arg	Pro 25 Thr Glu Ser Gly Val 105 Cys	ID NO Leu 10 Gly Gly Met Asp His 90 Ser Leu	Glu Ser Met Glu Asp 75 His Leu Ser	Cys Ser Cys Phe 60 Pro Ala Met Leu Ile	Asp Thr 45 Leu Ser Arg Cys Pro 125	Ser 30 His Val Leu Pro 110 Lys	15 Pro Ala Val Ser Cys 95 Ser	Ala Arg Gly Ala 80 Leu Trp	
175 176 178 180 182 183 185 186 189 191 192 194 195 197 198 200 201 203 204 206 207	Met 1 Ser Ser Leu Gln 65 Ser Ala Ser	(xi Glu Ala Ala Ile 50 Ala Gln Asn Pro Tyr 130	(II (II) MOI) SEO Phe His Ser 35 Leu Gly Ser Phe Glu 115 Arg	Arg Pro Tyr Leu Ala Cys 100 Leu Arg	PPE: DPOLC DPOLC LE TY LE DI Leu 5 Asn Val Phe Glu Arg 85 Gly Lys Ala	amir DGY: YPE: ESCRI Leu Leu Ala Phe Leu 70 Tyr Arg Gln	line protection and line protection arg leu 55 pro Arg Asn Ser Val 135	cid ear tein DN: S Pro Leu Ile 40 Val Thr Thr Arg Thr 120 Pro	Pro 25 Thr Glu Ser Gly Val 105 Cys Gly	ID NO Leu 10 Gly Gly Met Asp His 90 Ser Leu	Ser Met Glu Asp 75 His Leu Ser Phe	Cys Ser Cys Phe 60 Pro Ala Met Leu Ile 140	Asp Thr 45 Leu Ser Arg Cys Pro 125 Leu	Ser 30 His Wal Leu Pro 110 Lys	15 Pro Ala Val Ser Cys 95 Ser Cys	Ala Arg Gly Ala 80 Leu Trp Trp Leu	



Input Set : A:\PTO.txt

210	115					150					155					160	
	145			T	~1		G =	m1	D	~1		T	772 -	D	D		
	HIS	ser	ser	Leu		PIO	ser	THE	PIO		116	гус	HIS	PIO	Pro	Ald	
213	~		G	01	165		C 1	m1	T	170	1 /- ±	TT -	TT -	m	175	m	
	ser	Ата	ser		vaı	Ата	GIY	Thr		Asp	мет	HIS	HIS		Thr	Trp	
216	_	-1.		180	51 .	~ 1	51	_	185	_	_	a 1	_	190	•	_	
	Leu	TTE		IIe	Pne	тте	Pne		Pne	ьeu	Arg	GIn		Leu	Asn	Ser	
219			195					200	_	_	_		205	_		_	
	Val		GIn	Ala	GLY	Val		Trp	Arg	Asn	Leu	_	Ser	Leu	Gln	Pro	
222		210				_	215			_		220	_			_	
		Pro	Pro	Gly	Phe	_	Leu	Phe	Ser	Cys		Ser	Leu	Leu	Ser		
	225					230					235					240	
	Trp	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu		Asn	Phe	Phe	Val	Phe	Leu	
228					245			_		250					255		
230	Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arg	Leu	Ile	Leu	Ile	Ser	Gly	
231				260					265					270			
233	Pro	Cys	Asp	Leu	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	Gly	Ile	Thr	Gly	
234			275					280					285				
236	Val	Ser	His	His	Ala	Arg	Leu	Ile	Phe	Asn	Phe	Cys	Leu	Phe	Glu	Met	
237		290					295					300					
239	Glu	Ser	His	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Pro	Asn	Leu	Gly	
240	305					310					315					320	
242	Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu	Lys	Arg	Phe	Ser	Cys	Leu	Ser	
243					325					330					335		
245	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Gly	His	Leu	Pro	Pro	His	Pro	Ala	Asn	
246				340	-	_	-	-	345					350			
248	Phe	Cys	Ile	Phe	Ile	Arq	Gly	Gly	Val	Ser	Pro	Tyr	Leu	Ser	Gly	Trp	
249		-	355			_	-	360				-	365	•	•	-	
251	Ser	Gln	Thr	Pro	Asp	Leu	Arg										
252		370			-		375										
254	(2)	INFO	ORMA!	rion	FOR	SEQ	ID 1	NO: 3	3:								
256	• •						CTER										
257		•							pair	rs							
258			-	-			Leic										
259							ESS:										
260			•	•			both										
262		(ii)	•	•			CDN										
267									SEQ :	ID NO) : 3	:					
													AGTO	GCA A	ATGG	CGCAAT	60
																CTCCCC	120
																TTAGTA	180
																ATGATC	240
																GCCTC	300
																STCTCC	360
																CAGCC	420
																CAGGAT	480
																CAATCC	540
																GTAATT	600
																GAGTGC	660
																CCTGCC	720
Z 9 1	AGI		AA .	CIIC	CIC	JA C	LGCAR	rcc1(- 16(1	JUGG	GII	JAAG'.	LIA :	LICI	CIGCC	/20

RAW SEQUENCE LISTING DATE: 10/16/2001 PATENT APPLICATION: US/09/964,666 TIME: 15:20:47

Input Set : A:\PTO.txt

293	CCAGCCTCCT GAGTAGCTGG GACTACAGGC	GCCCACCACG	CCTAGCTAAT	TTTTTTGTAT	780
295	TTTTAGTAGA GATGGGGTTT CACCATGTTC	GCCAGGTTGA	TCTTGATCTC	TTGACCTTGT	840
297	GATCTGCCTG CCTCGGCCTA CCCAAAGTGC	TGGGATTACA	GGTCGTGACT	CCACGCCGGC	900
299	CTATTTTAA TTTTTGTTTG TTTGAAATGG	AATCTCACTC	TGTTACCCAG	GTCGGAGTGC	960
301	AATGGCAAAT CTCGGCTACT CGCAACCTCT	GCCTCCCGGG	TCAAGCGATT	CTCCTGTCTC	1020
303	AGCCTCCCAA GCAGCTGGGA TTACGGGACC	TGCACCACAC	CCCGCTAATT	TTTGTATTTT	1080
305	CATTAGAGGC GGGTTTACCA TATTTGTCAG	GCTGGGTCTC	AAACTCCTGA	CCTCAGGTGA	1140
307	CCCACCTGCC TCAGCCTTCC AAAGTGCTGG	GATTACAGGC	GTGAGCCACC	TCACCCAGCC	1200
309	GGCTAATTTG GAATAAAAA TATGTAGCAA	TGGGGGTCTG	CTATGTTGCC	CAGGCTGGTC	1260
311	TCAAACTTCT GGCTTCAGTC AATCCTTCCA	AATGAGCCAC	AACACCCAGC	CAGTCACATT	1320
313	TTTTAAACAG TTACATCTTT ATTTTAGTAI	ACTAGAAAGT	AATACAATAA	ACATGTCAAA	1380
315	C				1381
317	(2) INFORMATION FOR SEQ ID NO: 4	:			
319	(i) SEQUENCE CHARACTERISTIC	S:			
320	(A) LENGTH: 1418 base	pairs			
321	(B) TYPE: nucleic acid	l			
322	(C) STRANDEDNESS: both	ı			
323	(D) TOPOLOGY: both				
325	(ii) MOLECULE TYPE: cDNA				
330	(xi) SEQUENCE DESCRIPTION: S	EQ ID NO: 4	:		
332	TTTTTTTTT GAGATGGAGT TTTCGCTCTT	GTTGCCCAGG	CTGGAGTGCA	ATGGCGCAAT	60
334	CTCAGCTCAC CGCAACCTCC GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
336	AGTAGGCTGG GATTACAGGC ATGTGCACCA	CGCTCGGCTA	ATTTTGTATT	TTTTTTTAGT	180
338	AGAGATGGAG TTTCTCCATG TTGGTCAGGC	TGGTCTCGAA	CTCCGACCTC	AGATGATCCT	240
340	CCCGTCTCGG CCTCCCAAAG TGCTAGATAC	AGGACTGAGC	ACCATGCCCG	GCCTCTGCCT	300
342	GGCTAATTTT TGTGGTAGAA ACAGGGTTTC	ACTGATGTGC	CCAAGCTGGT	CTCCTGAGCT	360
344	CAAGCAGTCC ACCTGCCTCA GCCTCCCAAA	GTGCTGGGAT	TACAGGCGTG	CAGCCGTGCC	420
346	TGGCCTTTTT ATTTTATTTT TTTTAAGACA	CAGGTGTCCC	ACTCTTACCC	AGGATGAAGT	480
349	GCAGTGGTGT GATCACAGCT CACTGCAGCC	TTCAACTCTG	AGATCAAGCA	TCCTCCTGCC	540
	TCAGCCTCCC AAAGTAGCTG GGACCAAAGA				600
353	TTTTATTTTT AATTTTTTGA GACAGAGTCT	CAACTCTGTC	ACCCAGGCTG	GAGTGCAGTG	660
	GCGCAATCTT GGCTCACTGC AACCTCTGCC				720
	CCTCCTGAGT AGCTGGGACT ACAGGCGCCC				780
	AGTAGAGATG, GGGTTTCACC ATGTTCGCCA				840
	CTGCCTGCCT CGGCCTCCCA AAGTGCTGGG				900
	TATTTTTAAT TTTTGTTTGT TTGAAATGGA				960
	ATGGCCAAAT CTCGGCTCAC TGCAACCTCT				1020
	CAGCCTCCCA AGCAGCTGGG ATTACGGGCA				1080
	TTCATTAGAG GCGGGGTTTC ACCATATTTG				1140
	TGACCCACCT GCCTCAGCCT TCCAAAGTGC				1200
	CGGCTAATTT AGATAAAAAA ATATGTAGCA				1260
	GTCTCAAACT TCTGGCTTCA TGCAATCCTT				1320
	ATTTTTAAAC AGTTACATCT TTATTTTAGT		GTGATACGAT	AACATGGCGG	1380
	AACCTGCAAA TTCGAGTAGT ACAGAGTCTT				1418
	(2) INFORMATION FOR SEQ ID NO: 5				
383	(i) SEQUENCE CHARACTERISTIC				
384	(A) LENGTH: 22 base pa				
385	(B) TYPE: nucleic acid				
386	(C) STRANDEDNESS: sing	ıe			

VERIFICATION SUMMARY

DATE: 10/16/2001

PATENT APPLICATION: US/09/964,666

TIME: 15:20:48

Input Set : A:\PTO.txt

Output Set: N:\CRF3\10162001\I964666.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]